



OPIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/888,320

DATE: 02/21/2002
TIME: 12:01:24

Input Set : A:\Nih413-1.app
Output Set: N:\CRF3\02212002\I888320.raw

3 <110> APPLICANT: Barry III, Clifton E.
 4 DeBarber, Andrea E.
 5 Mdluli, Khismuzi
 6 Bekker, Linda-Gail
 7 The Government of the United States of America
 8 as represented by The Secretary of the
 9 Department of Health and Human Services

Does Not Comply
Corrected Diskette Needed
✓ and

11 <120> TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
 13 <130> FILE REFERENCE: 015280-413100US
 15 <140> CURRENT APPLICATION NUMBER: US 09/888,320
 16 <141> CURRENT FILING DATE: 2001-06-22
 18 <150> PRIOR APPLICATION NUMBER: US 60/214,187
 19 <151> PRIOR FILING DATE: 2000-06-26
 21 <160> NUMBER OF SEQ ID NOS: 16
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1867
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mycobacterium tuberculosis
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (201)..(1670)
 36 <223> OTHER INFORMATION: EtaA
 38 <400> SEQUENCE: 1
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 43 gtcaccctgg cagcttacta cgtgtcgata gtgtcgacat ctgcgttgacg gcctcgacat 180
 45 tacgttgata gcgtggatcc atg acc gag cac ctc gac gtt gtc atc gtg ggc 233
 46 Met Thr Glu His Leu Asp Val Val Ile Val Gly
 47 1 5 10
 49 gct gga atc tcc ggt gtc agc gcg gcc tgg cac ctg cag gac cgt tgc 281
 50 Ala Gly Ile Ser Gly Val Ser Ala Ala Trp His Leu Gln Asp Arg Cys
 51 15 20 25
 53 ccg acc aag agc tac gcc atc ctg gaa aag cgg gaa tcc atg ggc ggc 329
 54 Pro Thr Lys Ser Tyr Ala Ile Leu Glu Lys Arg Glu Ser Met Gly Gly
 55 30 35 40
 57 acc tgg gat ttg ttc cgt tat ccc gga att cgc tcc gac tcc gac atg 377
 58 Thr Trp Asp Leu Phe Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met
 59 45 50 55
 61 tac acg cta ggt ttc cga ttc cgt ccc tgg acc gga cgg cag gcg atc 425
 62 Tyr Thr Leu Gly Phe Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile

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63	60	65	70	75													
65	gcc	gac	ggc	aag	ccc	atc	ctc	gag	tac	gtc	aag	agc	acc	gcc	gca	atg	473
66	Ala	Asp	Gly	Lys	Pro	Ile	Leu	Glu	Tyr	Val	Lys	Ser	Thr	Ala	Ala	Met	
67																	
69	tat	gga	atc	gac	agg	cat	atc	cg	tgc	cac	cac	aag	gtg	atc	agt	gcc	521
70	Tyr	Gly	Ile	Asp	Arg	His	Ile	Arg	Phe	His	His	Lys	Val	Ile	Ser	Ala	
71																	
73	gat	tgg	tcg	acc	gca	gaa	aac	cgc	tgg	acc	cac	atc	caa	agc	cac		569
74	Asp	Trp	Ser	Thr	Ala	Glu	Asn	Arg	Trp	Thr	Val	His	Ile	Gln	Ser	His	
75																	
77	ggc	acg	ctc	agc	gcc	ctc	acc	tgc	gaa	ttc	ctc	ttt	ctg	tgc	agc	ggc	617
78	Gly	Thr	Leu	Ser	Ala	Leu	Thr	Cys	Glu	Phe	Leu	Phe	Leu	Cys	Ser	Gly	
79																	
81	tac	tac	aat	tac	gac	gag	ggc	tac	tgc	ccg	aga	ttc	gcc	ggc	tgc	gag	665
82	Tyr	Tyr	Asn	Tyr	Asp	Glu	Gly	Tyr	Ser	Pro	Arg	Phe	Ala	Gly	Ser	Glu	
83	140																155
85	gat	ttc	gtc	ggg	ccg	atc	atc	cat	ccg	cag	cac	tgg	ccc	gag	gac	ctc	713
86	Asp	Phe	Val	Gly	Pro	Ile	Ile	His	Pro	Gln	His	Trp	Pro	Glu	Asp	Leu	
87																	
89	gac	tac	gac	gct	aag	aac	atc	gtc	gtg	atc	ggc	agt	ggc	gca	acg	gca	761
90	Asp	Tyr	Asp	Ala	Lys	Asn	Ile	Val	Val	Ile	Gly	Ser	Gly	Ala	Thr	Ala	
91																	
93	gtc	acg	ctc	gtg	ccg	gca	ctg	gca	gac	tcg	ggc	gcc	aag	cac	gtc	acg	809
94	Val	Thr	Leu	Val	Pro	Ala	Leu	Ala	Asp	Ser	Gly	Ala	Lys	His	Val	Thr	
95																	
97	atg	ctg	cag	ccg	tca	ccc	acc	tac	atc	gtg	tcg	cag	cca	gac	ccg	gac	857
98	Met	Leu	Gln	Arg	Ser	Pro	Thr	Tyr	Ile	Val	Ser	Gln	Pro	Asp	Arg	Asp	
99																	
101	ggc	atc	gcc	gag	aag	aat	ctc	acg	tcg	ccg	gag	acc	atg	gcc	tac		905
102	Gly	Ile	Ala	Glu	Lys	Leu	Asn	Arg	Trp	Leu	Pro	Glu	Thr	Met	Ala	Tyr	
103	220																235
105	acc	gca	gtt	ccg	tgg	aag	aac	gtg	ctg	ccg	cag	gca	gtt	tac	acg		953
106	Thr	Ala	Val	Arg	Trp	Lys	Asn	Val	Leu	Arg	Gln	Ala	Ala	Val	Tyr	Ser	
107																	
109	gcc	tgc	cag	aag	tgg	cca	ccg	ccg	atg	ccg	aag	atg	ttc	ctg	agc	ctg	1001
110	Ala	Cys	Gln	Lys	Trp	Pro	Arg	Arg	Met	Arg	Lys	Met	Phe	Leu	Ser	Leu	
111																	
113	atc	cag	ccg	cag	cta	ccc	gag	ggg	tac	gac	gtg	cga	aag	cac	ttc	ggc	1049
114	Ile	Gln	Arg	Gln	Leu	Pro	Glu	Gly	Tyr	Asp	Val	Arg	Lys	His	Phe	Gly	
115																	
117	ccg	cac	tac	aat	ccc	tgg	gac	cag	cga	ttg	tcg	gtg	ccc	aac	ggc		1097
118	Pro	His	Tyr	Asn	Pro	Trp	Asp	Gln	Arg	Leu	Cys	Leu	Val	Pro	Asn	Gly	
119																	
121	gac	ctg	ttc	cg	gcc	att	cgt	cac	ggg	aag	gtc	gag	gtg	gtg	acc	gac	1145
122	Asp	Leu	Phe	Arg	Ala	Ile	Arg	His	Gly	Lys	Val	Glu	Val	Val	Thr	Asp	
123	300																315
125	acc	att	gaa	cg	ttc	acc	gca	acc	gga	atc	cg	ctg	aac	tca	ggt	cg	1193
126	Thr	Ile	Glu	Arg	Phe	Thr	Ala	Thr	Gly	Ile	Arg	Leu	Asn	Ser	Gly	Arg	
127																	

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129	gaa	ctg	ccg	gct	gac	atc	atc	att	acc	gca	acg	ggg	ttg	aac	ctg	cag	1241
130	Glu	Leu	Pro	Ala	Asp	Ile	Ile	Ile	Thr	Ala	Thr	Gly	Leu	Asn	Leu	Gln	
131				335					340					345			
133	ctt	ttt	ggg	gca	acg	gcg	act	atc	gac	gga	caa	caa	gtg	gac	atc		1289
134	Leu	Phe	Gly	Gly	Ala	Thr	Ala	Thr	Ile	Asp	Gly	Gln	Gln	Val	Asp	Ile	
135				350					355					360			
137	acc	acg	acg	atg	gcc	tac	aag	ggc	atg	atg	ctt	tcc	ggc	atc	ccc	aac	1337
138	Thr	Thr	Thr	Met	Ala	Tyr	Lys	Gly	Met	Met	Leu	Ser	Gly	Ile	Pro	Asn	
139				365					370			375					
141	atg	gcc	tac	acg	gtt	ggc	tac	acc	aat	gcc	tcc	tgg	acg	ctg	aag	gcc	1385
142	Met	Ala	Tyr	Thr	Val	Gly	Tyr	Thr	Asn	Ala	Ser	Trp	Thr	Leu	Lys	Ala	
143	380				385						390				395		
145	gac	ctg	gtg	tcg	gag	ttt	gtc	tgt	cgc	ttg	ttg	aat	tac	atg	gac	gac	1433
146	Asp	Leu	Val	Ser	Glu	Phe	Val	Cys	Arg	Leu	Leu	Asn	Tyr	Met	Asp	Asp	
147						400				405					410		
149	aac	ggt	ttt	gac	acc	gtg	gtc	gtc	gag	cga	ccg	ggc	tca	gat	gtc	gaa	1481
150	Asn	Gly	Phe	Asp	Thr	Val	Val	Val	Glu	Arg	Pro	Gly	Ser	Asp	Val	Glu	
151						415				420				425			
153	gag	cg	ccc	ttc	atg	gag	ttc	acc	cca	gg	tac	gtg	ctg	cgc	tcg	ctg	1529
154	Glu	Arg	Pro	Phe	Met	Glu	Phe	Thr	Pro	Gly	Tyr	Val	Leu	Arg	Ser	Leu	
155					430				435				440				
157	gac	gag	ctg	ccc	aag	cag	gg	tcg	cgt	aca	ccg	tgg	cgc	ctg	aat	cag	1577
158	Asp	Glu	Leu	Pro	Lys	Gln	Gly	Ser	Arg	Thr	Pro	Trp	Arg	Leu	Asn	Gln	
159					445				450			455					
161	aac	tac	cta	cgt	gac	atc	cg	ctc	atc	cg	cg	ggc	aag	atc	gac	gac	1625
162	Asn	Tyr	Leu	Arg	Asp	Ile	Arg	Leu	Ile	Arg	Arg	Gly	Lys	Ile	Asp	Asp	
163	460					465				470					475		
165	gag	gg	ctg	cg	ttc	gcc	aaa	agg	cct	gcc	ccg	gtg	ggg	gtt	tag		1670
166	Glu	Gly	Leu	Arg	Phe	Ala	Lys	Arg	Pro	Ala	Pro	Val	Gly	Val			
167						480				485				490			
169	ctttagcgac	gg	tttagcg	cg	tttaggc	cata	gtc	aga	cg	acgtat	gtat	gg	ccgtcgtc	g	ccgtcgtc	1730	
171	tcg	ctgt	agg	cg	atatcg	cc	cg	aaacg	aa	gtc	accc	cg	cc	agcgt	gtat	ttcaacgtc	1790
173	cgtt	ctcc	cg	cac	cggt	tctt	gg	tgc	gtt	cg	gggg	att	gg	tg	ccc	agcgc	1850
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188					20					25				30			
189	Ala	Ile	Leu	Glu	Lys	Arg	Glu	Ser	Met	Gly	Gly	Thr	Trp	Asp	Leu	Phe	
190				35					40				45				
191	Arg	Tyr	Pro	Gly	Ile	Arg	Ser	Asp	Ser	Asp	Met	Tyr	Thr	Leu	Gly	Phe	
192				50					55			60					
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194	65	70	75	80												
195	Ile	Leu	Glu	Tyr	Val	Lys	Ser	Thr	Ala	Ala	Met	Tyr	Gly	Ile	Asp	Arg
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197	His	Ile	Arg	Phe	His	His	Lys	Val	Ile	Ser	Ala	Asp	Trp	Ser	Thr	Ala
198								100				105				110
199	Glu	Asn	Arg	Trp	Thr	Val	His	Ile	Gln	Ser	His	Gly	Thr	Leu	Ser	Ala
200								115				120				125
201	Leu	Thr	Cys	Glu	Phe	Leu	Phe	Leu	Cys	Ser	Gly	Tyr	Tyr	Asn	Tyr	Asp
202								130				135				140
203	Glu	Gly	Tyr	Ser	Pro	Arg	Phe	Ala	Gly	Ser	Glu	Asp	Phe	Val	Gly	Pro
204								145				150				160
205	Ile	Ile	His	Pro	Gln	His	Trp	Pro	Glu	Asp	Leu	Asp	Tyr	Asp	Ala	Lys
206								165				170				175
207	Asn	Ile	Val	Val	Ile	Gly	Ser	Gly	Ala	Thr	Ala	Val	Thr	Leu	Val	Pro
208								180				185				190
209	Ala	Leu	Ala	Asp	Ser	Gly	Ala	Lys	His	Val	Thr	Met	Leu	Gln	Arg	Ser
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211	Pro	Thr	Tyr	Ile	Val	Ser	Gln	Pro	Asp	Arg	Asp	Gly	Ile	Ala	Glu	Lys
212								210				215				220
213	Leu	Asn	Arg	Trp	Leu	Pro	Glu	Thr	Met	Ala	Tyr	Thr	Ala	Val	Arg	Trp
214								225				230				240
215	Lys	Asn	Val	Leu	Arg	Gln	Ala	Ala	Val	Tyr	Ser	Ala	Cys	Gln	Lys	Trp
216								245				250				255
217	Pro	Arg	Arg	Met	Arg	Lys	Met	Phe	Leu	Ser	Leu	Ile	Gln	Arg	Gln	Leu
218								260				265				270
219	Pro	Glu	Gly	Tyr	Asp	Val	Arg	Lys	His	Phe	Gly	Pro	His	Tyr	Asn	Pro
220								275				280				285
221	Trp	Asp	Gln	Arg	Leu	Cys	Leu	Val	Pro	Asn	Gly	Asp	Leu	Phe	Arg	Ala
222								290				295				300
223	Ile	Arg	His	Gly	Lys	Val	Glu	Val	Val	Thr	Asp	Thr	Ile	Glu	Arg	Phe
224								305				310				320
225	Thr	Ala	Thr	Gly	Ile	Arg	Leu	Asn	Ser	Gly	Arg	Glu	Leu	Pro	Ala	Asp
226								325				330				335
227	Ile	Ile	Ile	Thr	Ala	Thr	Gly	Leu	Asn	Leu	Gln	Leu	Phe	Gly	Gly	Ala
228								340				345				350
229	Thr	Ala	Thr	Ile	Asp	Gly	Gln	Gln	Val	Asp	Ile	Thr	Thr	Thr	Met	Ala
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231	Tyr	Lys	Gly	Met	Met	Leu	Ser	Gly	Ile	Pro	Asn	Met	Ala	Tyr	Thr	Val
232								370				375				380
233	Gly	Tyr	Thr	Asn	Ala	Ser	Trp	Thr	Leu	Lys	Ala	Asp	Leu	Val	Ser	Glu
234								385				390				400
235	Phe	Val	Cys	Arg	Leu	Leu	Asn	Tyr	Met	Asp	Asp	Asn	Gly	Phe	Asp	Thr
236								405				410				415
237	Val	Val	Val	Glu	Arg	Pro	Gly	Ser	Asp	Val	Glu	Glu	Arg	Pro	Phe	Met
238								420				425				430
239	Glu	Phe	Thr	Pro	Gly	Tyr	Val	Leu	Arg	Ser	Leu	Asp	Glu	Leu	Pro	Lys
240								435				440				445
241	Gln	Gly	Ser	Arg	Thr	Pro	Trp	Arg	Leu	Asn	Gln	Asn	Tyr	Leu	Arg	Asp
242								450				455				460

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243 Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp Glu Gly Leu Arg Phe
244 465 470 475 480
245 Ala Lys Arg Pro Ala Pro Val Gly Val
246 485
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255 <220> FEATURE:
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257 amplification primer
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260 ggggttaccga cattacgttg atagcgtgga 30
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265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
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272 <400> SEQUENCE: 4
273 ataagaatgc ggccgcaacc gtcgctaaag ctaaacc 37
276 <210> SEQ ID NO: 5
277 <211> LENGTH: 18
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
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283 sequencing primer, EtaA amplification primer
285 <400> SEQUENCE: 5 18
286 atcatccatc cgtagcac
289 <210> SEQ ID NO: 6
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291 <212> TYPE: DNA
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303 <211> LENGTH: 17
304 <212> TYPE: DNA
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309 sequencing primer, EtaA amplification primer
311 <400> SEQUENCE: 7
312 gcatcgtgac gtgcttg 17

VERIFICATION SUMMARY

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L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1